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Application No: 10522106 Version No: 1.0

Input Set:

Output Set:

Started: 2007-08-21 07:56:35.977
Finished: 2007-08-21 07:56:38.925
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 948 ms
Total Warnings: 2
Total Errors: 0
No. of SeqIDs Defined: 24
Actual SeqID Count: 24

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)

SEQUENCE LISTING

<110> Kogel, Karl-Heinz
Huckelhoven, Ralph
Trujillo, Marco

<120> Method for Obtaining the pathogenic resistance in plants

<130> 12810-00067-US

<140> 10522106

<141> 2007-08-21

<160> 24

<170> PatentIn version 3.3

<210> 1

<211> 337

<212> DNA

<213> Hordeum vulgare

<220>

<221> CDS

<222> (2)..(337)

<223> coding for NADPH oxidase (fragment)

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Phe Lys Gly Ile Met Asn Glu Ile Ala Glu Leu Asp Gln Arg Asn Ile
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att gag atg cac aac tat ctc aca agt gtt tat gag gaa ggg gat gct 97
Ile Glu Met His Asn Tyr Leu Thr Ser Val Tyr Glu Glu Gly Asp Ala
20 25 30
cgg tca gca ctc atc aca atg ctg caa gct ctc aac cat gcc aag aat 145
Arg Ser Ala Leu Ile Thr Met Leu Gln Ala Leu Asn His Ala Lys Asn
35 40 45
ggt gtc gat gta gtg tct ggm act cga gtc cg^g aca cat ttt gca aga 193
Gly Val Asp Val Val Ser Xaa Thr Arg Val Arg Thr His Phe Ala Arg
50 55 60
cca aat ttt aag agg gtg ctg tct aag gta gcc gcc aaa cat cct tat 241
Pro Asn Phe Lys Arg Val Leu Ser Lys Val Ala Ala Lys His Pro Tyr
65 70 75 80
gcc aag ata gga gtg ttc tat tgc gga gct cca gtt ctg gc^g cag gaa 289
Ala Lys Ile Gly Val Phe Tyr Cys Gly Ala Pro Val Leu Ala Gln Glu
85 90 95
cta agc aac ctt tgc cat gag ttc aat ggc aaa tgc acg aca aaa ttc 337
Leu Ser Asn Leu Cys His Glu Phe Asn Gly Lys Cys Thr Thr Lys Phe
100 105 110

<210> 2

<211> 112

<212> PRT

<213> Hordeum vulgare

<220>

<221> misc_feature

<222> (55)..(55)

<223> The 'Xaa' at location 55 stands for Gly.

<400> 2

Phe Lys Gly Ile Met Asn Glu Ile Ala Glu Leu Asp Gln Arg Asn Ile
1 5 10 15
Ile Glu Met His Asn Tyr Leu Thr Ser Val Tyr Glu Glu Gly Asp Ala
20 25 30
Arg Ser Ala Leu Ile Thr Met Leu Gln Ala Leu Asn His Ala Lys Asn
35 40 45
Gly Val Asp Val Val Ser Xaa Thr Arg Val Arg Thr His Phe Ala Arg
50 55 60
Pro Asn Phe Lys Arg Val Leu Ser Lys Val Ala Ala Lys His Pro Tyr
65 70 75 80
Ala Lys Ile Gly Val Phe Tyr Cys Gly Ala Pro Val Leu Ala Gln Glu
85 90 95
Leu Ser Asn Leu Cys His Glu Phe Asn Gly Lys Cys Thr Thr Lys Phe
100 105 110

<210> 3

<211> 2832

<212> DNA

<213> Oryza sativa

<220>

<221> CDS

<222> (1)..(2829)

<223> coding for NADPH oxidase

<400> 3

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1 5 10 15
acg aca ccg cgg tcg ctg acg acg ggc tcg tcg ccg cgc ggg tcc gac 96
Thr Thr Pro Arg Ser Leu Ser Thr Gly Ser Ser Pro Arg Gly Ser Asp
20 25 30
gac cgg agc tcc gac gac ggg gag gag ctg gtc gag gtc acg ctc gac 144
Asp Arg Ser Ser Asp Asp Gly Glu Glu Leu Val Glu Val Thr Leu Asp
35 40 45
ctg cag gac gac acc att gtg ctt cgg agc gtc gag ccc gcg gcg 192
Leu Gln Asp Asp Asp Thr Ile Val Leu Arg Ser Val Glu Pro Ala Ala
50 55 60
gcg gcg gcg gcg ggg gtg ggg gcg ggg gcg ggg gcg gcg tcg gcg cgg 240
Ala Ala Ala Ala Gly Val Gly Ala Gly Ala Ala Ser Ala Arg
65 70 75 80
ggg gag ctc acg ggt ggc ccg tcg tcg tcg tcg cgg tcg agg tcg 288
Gly Glu Leu Thr Gly Gly Pro Ser Ser Ser Ser Arg Ser Arg Ser
85 90 95
ccg tcg atc cgg agg agc tcg tcg cac ccg ctg cag ttc tcg cag 336
Pro Ser Ile Arg Arg Ser Ser Ser His Arg Leu Leu Gln Phe Ser Gln
100 105 110
gag ctc aag gcg gag gcc atg gcc ccg gcg ccg cag ttc tcg cag gac 384
Glu Leu Lys Ala Glu Ala Met Ala Arg Ala Arg Gln Phe Ser Gln Asp
115 120 125
ctg acc aag cgg ttc ggc cgc agc cac agc cgc agc gaa gcg cag gcg 432
Leu Thr Lys Arg Phe Gly Arg Ser His Ser Arg Ser Glu Ala Gln Ala
130 135 140

ccg tcc ggc ctc gag tcc gcg ctc gcc gcc cgcc ggc gcg cgg cgg cag 480
 Pro Ser Gly Leu Glu Ser Ala Leu Ala Ala Arg Ala Ala Arg Arg Gln
 145 150 155 160
 cgc gcg cag ctc gac cgc aca cgc tcc ggc gcc cac aag gcg ctc cgc 528
 Arg Ala Gln Leu Asp Arg Thr Arg Ser Gly Ala His Lys Ala Leu Arg
 165 170 175
 ggc ctc cgc ttc atc agc agc aac aag gcc aac aac gcc tgg atg gag 576
 Gly Leu Arg Phe Ile Ser Ser Asn Lys Ala Asn Asn Ala Trp Met Glu
 180 185 190
 gtg cag gcc aac ttc gac cgc ctc gcc cgc gac ggc tac ctc tcc cgc 624
 Val Gln Ala Asn Phe Asp Arg Leu Ala Arg Asp Gly Tyr Leu Ser Arg
 195 200 205
 tcc gac ttc gcc gaa tgc atc ggg atg acg gaa tgc aag gag ttc gcg 672
 Ser Asp Phe Ala Glu Cys Ile Gly Met Thr Glu Ser Lys Glu Phe Ala
 210 215 220
 ctc gag ctg ttc gac acg ctg agc cgg cga cga cag atg aag gtg gac 720
 Leu Glu Leu Phe Asp Thr Leu Ser Arg Arg Gln Met Lys Val Asp
 225 230 235 240
 acg att aac aag gat gaa ctc cgc gag atc tgg cag cag atc acc gat 768
 Thr Ile Asn Lys Asp Glu Leu Arg Glu Ile Trp Gln Gln Ile Thr Asp
 245 250 255
 aac agc ttc gac tcc cgt ctc caa atc ttc ttc gaa atg gtg gat aag 816
 Asn Ser Phe Asp Ser Arg Leu Gln Ile Phe Phe Glu Met Val Asp Lys
 260 265 270
 aac gcg gac ggc cgg att acg gag gcg gag gtg aaa gag att att atg 864
 Asn Ala Asp Gly Arg Ile Thr Glu Ala Glu Val Lys Glu Ile Ile Met
 275 280 285
 ttg agc gcg tct gcc aat aaa ctg tcg agg ctt aag gag caa gca gaa 912
 Leu Ser Ala Ser Ala Asn Lys Leu Ser Arg Leu Lys Glu Gln Ala Glu
 290 295 300
 gag tac gcc gct ttg atc atg gag gag ctt gat cct gaa ggg ctc ggc 960
 Glu Tyr Ala Ala Leu Ile Met Glu Glu Leu Asp Pro Glu Gly Leu Gly
 305 310 315 320
 tac att gag cta tgg caa ttg gag aca ctt ctg ttg cag aaa gat acc 1008
 Tyr Ile Glu Leu Trp Gln Leu Glu Thr Leu Leu Leu Gln Lys Asp Thr
 325 330 335
 tat atg aac tat agt cag gcc ctt agt tac aca agc caa gca ctg agc 1056
 Tyr Met Asn Tyr Ser Gln Ala Leu Ser Tyr Thr Ser Gln Ala Leu Ser
 340 345 350
 cag aat ctt gca ggg cta agg aag aag agt tca atc cgc aaa ata agc 1104
 Gln Asn Leu Ala Gly Leu Arg Lys Lys Ser Ser Ile Arg Lys Ile Ser
 355 360 365
 acc tct tta agc tac tat ttc gag gac aac tgg aaa cgt tta tgg qtg 1152
 Thr Ser Leu Ser Tyr Tyr Phe Glu Asp Asn Trp Lys Arg Leu Trp Val
 370 375 380
 ctt gca ttg tgg att ggg ata atg gct gga ctg ttc acc tgg aaa ttc 1200
 Leu Ala Leu Trp Ile Gly Ile Met Ala Gly Leu Phe Thr Trp Lys Phe
 385 390 395 400
 atg cag tat cgt aac cga tat gtc ttt gat gtg atg ggc tac tgt gtc 1248
 Met Gln Tyr Arg Asn Arg Tyr Val Phe Asp Val Met Gly Tyr Cys Val
 405 410 415
 aca aca gca aaa gga gct gct gaa acc cta aag ctg aat atg gca att 1296
 Thr Thr Ala Lys Gly Ala Ala Glu Thr Leu Lys Leu Asn Met Ala Ile
 420 425 430
 atc ctc ctg cca gta tgc cgt aac acc att act tgg ttg cga agt aca 1344
 Ile Leu Leu Pro Val Cys Arg Asn Thr Ile Thr Trp Leu Arg Ser Thr
 435 440 445

agg gct gca cg	gca cta cct ttt gat gac aac atc aac ttc cac aag	1392	
Arg Ala Ala Arg Ala Leu Pro Phe Asp Asp Asn Ile Asn Phe His Lys			
450	455	460	
act att gca gca gca att gtg gtt ggt ata atc ctc cat gca ggg aac		1440	
Thr Ile Ala Ala Ala Ile Val Val Gly Ile Ile Leu His Ala Gly Asn			
465	470	475	480
cac ctt gta tgc gat ttt cca cgg tta ata aaa tca tca gat gag aag		1488	
His Leu Val Cys Asp Phe Pro Arg Leu Ile Lys Ser Ser Asp Glu Lys			
485	490	495	
tat gct cct ttg ggc cag tat ttt ggg gaa ata aag cca aca tat ttt		1536	
Tyr Ala Pro Leu Gly Gln Tyr Phe Gly Glu Ile Lys Pro Thr Tyr Phe			
500	505	510	
aca ttg gtc aaa gga gtg gag ggc atc act ggg gta atc atg gtt gta		1584	
Thr Leu Val Lys Gly Val Glu Gly Ile Thr Gly Val Ile Met Val Val			
515	520	525	
tgc atg ata att gct ttt act cta gca acc cgg tgg ttc cgc cgt agc		1632	
Cys Met Ile Ile Ala Phe Thr Leu Ala Thr Arg Trp Phe Arg Arg Ser			
530	535	540	
ttg gtt aag ctt cca agg cca ttt gac aaa ctg act ggc ttc aat gcc		1680	
Leu Val Lys Leu Pro Arg Pro Phe Asp Lys Leu Thr Gly Phe Asn Ala			
545	550	555	560
ttt tgg tat tct cat cat ctg ttc atc att gtg tat atc gcg ctc att		1728	
Phe Trp Tyr Ser His His Leu Phe Ile Ile Val Tyr Ile Ala Leu Ile			
565	570	575	
gtt cat gga gag tgt cta tac ctt att cat gtc tgg tac aga aga acg		1776	
Val His Gly Glu Cys Leu Tyr Leu Ile His Val Trp Tyr Arg Arg Thr			
580	585	590	
aca tgg atg tat ctt tca gtg cct gtt tgc ttg tat gta ggg gag agg		1824	
Thr Trp Met Tyr Leu Ser Val Pro Val Cys Leu Tyr Val Gly Glu Arg			
595	600	605	
att cta agg ttc ttc agg tct ggc agt tat tct gtc cgg cta ttg aag		1872	
Ile Leu Arg Phe Phe Arg Ser Gly Ser Tyr Ser Val Arg Leu Leu Lys			
610	615	620	
gtg gcc ata tat cca ggt aat gtt ttg aca ctg caa atg tcc aag cct		1920	
Val Ala Ile Tyr Pro Gly Asn Val Leu Thr Leu Gln Met Ser Lys Pro			
625	630	635	640
ccc acg ttc cgt tac aag agt gga caa tat atg ttt gtt caa tgt cca		1968	
Pro Thr Phe Arg Tyr Lys Ser Gly Gln Tyr Met Phe Val Gln Cys Pro			
645	650	655	
gca gtg tct ccc ttt gaa tgg cat ccc ttc tca att act tca gca cct		2016	
Ala Val Ser Pro Phe Glu Trp His Pro Phe Ser Ile Thr Ser Ala Pro			
660	665	670	
ggg gat gac tac ctc agc att cat gtt cga caa ctt ggt gat tgg aca		2064	
Gly Asp Asp Tyr Leu Ser Ile His Val Arg Gln Leu Gly Asp Trp Thr			
675	680	685	
cga gaa ctc aag aga gta ttt gct gca gct tgt gag ccc cca gcg ggt		2112	
Arg Glu Leu Lys Arg Val Phe Ala Ala Ala Cys Glu Pro Pro Ala Gly			
690	695	700	
ggt aaa agc ggc ctt ctt agg gca gat gag aca act aag aaa atc tta		2160	
Gly Lys Ser Gly Leu Leu Arg Ala Asp Glu Thr Thr Lys Lys Ile Leu			
705	710	715	720
ccc aag ctt ctg att gat gga ccg tat ggt tct cct gct cag gat tac		2208	
Pro Lys Leu Leu Ile Asp Gly Pro Tyr Gly Ser Pro Ala Gln Asp Tyr			
725	730	735	
agc aag tat gat gtt tta tta ctt gtt gga tta gga att ggt gcg aca		2256	
Ser Lys Tyr Asp Val Leu Leu Val Gly Leu Gly Ile Gly Ala Thr			
740	745	750	

ccc ttt att agc ata tta aaa gat ctt ctg aat aac atc atc aaa atg			2304
Pro Phe Ile Ser Ile Leu Lys Asp Leu Leu Asn Asn Ile Ile Lys Met			
755	760	765	
gag gaa gag gag gat gct tct act gat ctt tat cca cca atg ggt cggt			2352
Glu Glu Glu Asp Ala Ser Thr Asp Leu Tyr Pro Pro Met Gly Arg			
770	775	780	
aat aag cca cat gtt gat ctg ggc aca ctt atg acg att acc tca aga			2400
Asn Lys Pro His Val Asp Leu Gly Thr Leu Met Thr Ile Thr Ser Arg			
785	790	795	800
cca aag aag atc ttg aag acc aca aat gct tac ttt tac tgg gtc aca			2448
Pro Lys Lys Ile Leu Lys Thr Thr Asn Ala Tyr Phe Tyr Trp Val Thr			
805	810	815	
cgt gag caa ggc tct ttt gat tgg ttc aaa gga gtc atg aat gaa att			2496
Arg Glu Gln Gly Ser Phe Asp Trp Phe Lys Gly Val Met Asn Glu Ile			
820	825	830	
gct gac ttg gat caa agg aat atc att gag atg cac aac tac cta aca			2544
Ala Asp Leu Asp Gln Arg Asn Ile Ile Glu Met His Asn Tyr Leu Thr			
835	840	845	
agc gtc tat gag gag ggg gat gcc agg tca gca ctc atc acc atg ctc			2592
Ser Val Tyr Glu Glu Gly Asp Ala Arg Ser Ala Leu Ile Thr Met Leu			
850	855	860	
caa gct ctg aac cat gcc aag aat gga gtt gat att gtc tct ggg aca			2640
Gln Ala Leu Asn His Ala Lys Asn Gly Val Asp Ile Val Ser Gly Thr			
865	870	875	880
aaa gtc cgg aca cat ttt gca cga cca aat tgg aga aag gtc ctt tct			2688
Lys Val Arg Thr His Phe Ala Arg Pro Asn Trp Arg Lys Val Leu Ser			
885	890	895	
aaa att tcc tcc aag cat cca tat gcc aaa ata ggt gta ttc tac tgt			2736
Lys Ile Ser Ser Lys His Pro Tyr Ala Lys Ile Gly Val Phe Tyr Cys			
900	905	910	
gga gct cca gtc ctg gca caa gaa cta agc aaa ctt tgc cat gaa ttc			2784
Gly Ala Pro Val Leu Ala Gln Glu Leu Ser Lys Leu Cys His Glu Phe			
915	920	925	
aac ggg aaa tgc aca acg aag ttc gaa ttc cat aag gag cat ttc tga			2832
Asn Gly Lys Cys Thr Thr Lys Phe Glu Phe His Lys Glu His Phe			
930	935	940	

<210> 4
<211> 943
<212> PRT
<213> Oryza sativa

<400> 4

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35	40	45	
Leu Gln Asp Asp Asp Thr Ile Val Leu Arg Ser Val Glu Pro Ala Ala			
50	55	60	
Ala Ala Ala Ala Gly Val Gly Ala Gly Ala Gly Ala Ala Ser Ala Arg			
65	70	75	80
Gly Glu Leu Thr Gly Gly Pro Ser Ser Ser Ser Arg Ser Arg Ser			
85	90	95	
Pro Ser Ile Arg Arg Ser Ser Ser His Arg Leu Leu Gln Phe Ser Gln			
100	105	110	

Glu Leu Lys Ala Glu Ala Met Ala Arg Ala Arg Gln Phe Ser Gln Asp
115 120 125
Leu Thr Lys Arg Phe Gly Arg Ser His Ser Arg Ser Glu Ala Gln Ala
130 135 140
Pro Ser Gly Leu Glu Ser Ala Leu Ala Ala Arg Ala Ala Arg Arg Gln
145 150 155 160
Arg Ala Gln Leu Asp Arg Thr Arg Ser Gly Ala His Lys Ala Leu Arg
165 170 175
Gly Leu Arg Phe Ile Ser Ser Asn Lys Ala Asn Asn Ala Trp Met Glu
180 185 190
Val Gln Ala Asn Phe Asp Arg Leu Ala Arg Asp Gly Tyr Leu Ser Arg
195 200 205
Ser Asp Phe Ala Glu Cys Ile Gly Met Thr Glu Ser Lys Glu Phe Ala
210 215 220
Leu Glu Leu Phe Asp Thr Leu Ser Arg Arg Gln Met Lys Val Asp
225 230 235 240
Thr Ile Asn Lys Asp Glu Leu Arg Glu Ile Trp Gln Gln Ile Thr Asp
245 250 255
Asn Ser Phe Asp Ser Arg Leu Gln Ile Phe Phe Glu Met Val Asp Lys
260 265 270
Asn Ala Asp Gly Arg Ile Thr Glu Ala Glu Val Lys Glu Ile Ile Met
275 280 285
Leu Ser Ala Ser Ala Asn Lys Leu Ser Arg Leu Lys Glu Gln Ala Glu
290